

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Au-Young, Janice
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: U.S.
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0066 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: SCAH-1
  - (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Lys	Ile	Phe	Leu	Pro	Val	Leu	Leu	Ala	Ala	Leu	Leu	Gly	Val	Glu
1				5					10					15	
Arg	Ala	Ser	Ser	Leu	Met	Cys	Phe	Ser	Cys	Leu	Asn	Gln	Lys	Ser	Asn
			20					25					30		

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Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys  
35 40 45  
Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly  
50 55 60  
His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly  
65 70 75 80  
Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe  
85 90 95  
Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr  
100 105 110  
Leu Leu Gly Ala Gly Leu Leu Leu Ser Leu Xaa Pro Ala Leu Leu Arg  
115 120 125  
Phe Gly Pro  
130

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCAH-2
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln  
1 5 10 15  
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn  
20 25 30  
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys  
35 40 45  
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys  
50 55 60  
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly  
65 70 75 80  
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Xaa Ser Gly  
85 90 95  
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala  
100 105 110  
Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCAH-1
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NAGGANGGTG	GGGGACCCAN	GGGTCCAGAG	CGCAGTTCGG	GTCGGAGCTY	CGWCCAGGCT	60
GCTGGTACCT	GGGTCCGCCC	GGCGAGCAGG	ACAGGCTGCT	TTGGTTTGTG	ACCTCCAGGC	120
AGGACGGCCA	TCCTCTCCAG	AATGAAGATC	TTCTTGCCAG	TGCTGCTGGC	TGCCCTTCTG	180
GGTGTGGAGC	GAGCCAGCTC	GCTGATGTGC	TTCTCCTGCT	TGAACCAGAA	GAGCAATCTG	240
TACTGCCTGA	AGCCGACCAT	CTGCTCCGAC	CAGGACAAC	ACTGCGTGAC	TGTGTCTGCT	300
AGTGCCGCGA	TTGGGAATCT	CGTGACATTT	GGCCACAGCC	TGAGCAAGAC	CTGTTCCCCG	360
GCCTGCCCCA	TCCCAGAAGG	CGTCAATGTT	GGTGTGGCTT	CCATGGGCAT	CAGCTGCTGC	420
CAGAGCTTTC	TGTGCAATTT	CAGTGCGGCC	GATGGCGGGC	TGCGGGCAAG	CGTCACCCTG	480
CTGGGTGCCG	GGCTGCTGCT	GAGCCTGWTG	CCGGCCCTGC	TGCGGTTTGG	CCCCTGA	537

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCAH-2
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCATGA	AGGCTGTGCT	GCTTGCCCTG	TTGATGGCAG	GCTTGGCCCT	GCAGCCAGGC	60
ACTGCCCTGC	TGTGCTACTC	CTGCAAAGCC	CAGGTGAGCA	ACGAGGACTG	CCTGCAGGTG	120
GAGAACTGCA	CCCAGCTGGG	GGAGCAGTGC	TGGACCGCGC	GCATCCGCGC	AGTTGGCCTC	180
CTGACCGTCA	TCAGCAAAGG	CTGCAGCTTG	AACTGCGTGG	ATGACTCACA	GGACTACTAC	240
GTGGGCAAGA	AGAACATCAC	GTGCTGTGAC	ACCGACTTGT	GCAACGSCAG	CGGGGCCCAT	300
GCCCTGCAGC	CGGCTGCCGC	CATCCTTGCG	CTGCTCCCTG	CACTCGGCCT	GCTGCTCTGG	360
GGACCCGGCC	AGCTATAGGC	TCTGGGGGGC	CCCGMTGCAG	CCCACACTGG	GTGTGGTGCC	420
CCAAGGCCTC	TGTGSCACTC	CTMACAGACC	TGGGCCCAGT	GGGAGSCTGT	CTCTNGGTTC	480
CTGAGGCACA	TCCT					494

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 434660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ser Ala Thr Ser Asn Met Arg Val Phe Leu Pro Val Leu Leu Ala
 1          5          10          15
Ala Leu Leu Gly Met Glu Gln Val His Ser Leu Met Cys Phe Ser Cys
 20          25          30
Thr Asp Gln Lys Asn Asn Ile Asn Cys Leu Trp Pro Val Ser Cys Gln
 35          40          45
Glu Lys Asp His Tyr Cys Ile Thr Leu Ser Ala Ala Gly Phe Gly
 50          55          60
Asn Val Asn Leu Gly Tyr Thr Leu Asn Lys Gly Cys Ser Pro Ile Cys
 65          70          75          80
Pro Ser Glu Asn Val Asn Leu Asn Leu Gly Val Ala Ser Val Asn Ser
 85          90          95
Tyr Cys Cys Gln Ser Ser Phe Cys Asn Phe Ser Ala Ala Gly Leu Gly
 100          105          110
Leu Arg Ala Ser Ile Pro Leu Leu Gly Leu Gly Leu Leu Ser Leu
 115          120          125
Leu Ala Leu Leu Gln Leu Ser Pro
 130          135

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1199651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Ser Thr Thr Ser Ser Met Arg Val Phe Ser Ile Val Leu Gln Ala
 1          5          10          15
His Leu Leu Gly Val Glu Leu Val Pro Ser Leu Ile Cys Ser Ser Cys
 20          25          30
Thr His Gln Lys Ser Asn Ile Asn Pro Pro Trp Pro Val Ala Cys Lys
 35          40          45
Asp Thr Gly Asn Tyr Cys Ile Met Leu Phe Ser Ala Val Gly Phe Gly
 50          55          60
Asn Val Asn Leu Gly Tyr Thr Leu Asn Thr Gly Cys Ser Gln Ser Cys
 65          70          75          80
Pro His Glu Asn Ile Asn Ile Asn Pro Gly Val Ala Ser Val Asn Ser
 85          90          95
Tyr Gln Ser Ser Phe Cys Asn Phe Ser Asn Ala Cys Leu
 100          105

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1PEB01

(B) CLONE: 72518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGAAGCCG	ACCATCTGNT	CCGACCAGGN	CAACTACTGN	GTGACTGTGT	CTGCTAGTGC	60
CGGCATTTGG	AATCTTGTGC	CATTNGACA	CAGCCTNAGC	AAGACCTNTT	CCCCGGCCTN	120
NCCCATCCCA	GAAGGNGTCA	ATNATNGT				143

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1PLB02

(B) CLONE: 155838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGACAGGCT	GCTTTGGTTT	GTNACCTCCA	GGCAGGACGG	CCATCCTCTC	CAGAATGAAG	60
ATCTTCTTGC	CANTGCTGCT	GGCTGCCCTT	CTNGGTGTGG	AGCGAGCCAG	CTCGCTGATG	120
TGCTTCTCCT	GCTTNAACCA	GAAGAGCAAT	CTGTACTGCC	TGAAGCCGAC	CATCTGCTCC	180
GACCAGGNCA	ACTACT					196

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HNT2RAT01

(B) CLONE: 486681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTCGGGGAG	CTCGGCCAGG	CTGCTGGTAC	CTGCGTCCGC	CCGGCGAGCA	GGACAGGCTG	60
CTTTGGTTTG	TGACCTNCAG	GCAGGACGGC	CATCCTCTNC	AGAATGAAGA	TCTTCTTGCC	120
AGTGCTGCTG	GNTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TNGCTGATGT	GCTTCTTCTG	180
CTTGAACCAG	AAGAGCAATC	TGTACTGCTG	AAGCCGACCA	TCTGTTCGAC	CAGGNCAACT	240
ACTGCGTGAC	TGTGTCTGCT	AGTGNCGGCA	TTGGGAAT			278

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 604702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTTCGGGGA	GCTCGGCCAG	GCTGCTGGTA	CCTGCGTCCG	CCCGGCGAGC	AGGACAGGCT	60
GCTTTGGTTT	GTGACCTCCA	GGCAGGACGG	CCATCCTCTC	CAGAATGAAG	ATCTTCTTGC	120
CAGTGCTGCT	GGCTGCCCTT	CTGGGTGTGG	AGCGAGCCAG	CTCGCTGATG	TGCTTCTCCT	180
GCTTGAACCA	GAAGAGCAAT	CTGTACTGCC	TGAAGCCGAC	CATCTGCTCC	GACCAGGACA	240
ACTACTGCGT	GACTGTGTCT	GC				262

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 606246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTTCGGGGAG	CTCGGCCAGG	CTGCTGGTAC	CTGCGTCCGC	CCGGCGAGCA	GGACAGGCTG	60
CTTTGGTTTG	TGACCTCCAG	GCAGGACGGC	CATCCTCTCC	AGAATGAAGA	TCTTCTTGCC	120
AGTGCTGCTG	GCTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TCGCTGATGT	GCTTCTCCTG	180
CTTGAACCAG	AAGAGCAATC	TGTACTGCCT	GAAGCCGACC	ATCTGCTCCG	ACCAGGACAA	240
CTACTGCGTG	ACTGTGTCTG	CTAGTGCCGG	CATTGGGAAT	CTCGTGACA		289

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 637479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GTTCGGGGAG	CTCGGCCAGG	CTGCTGGTAC	CTGCGTCCGC	CCGGCGAGCA	GGACAGGCTG	60
CTTTGGTTTG	TGACCTCCAG	GCAGGACGGC	CATCCTNTCC	AGAATGAAGA	TCTTCTTGCC	120
AGTGCTGCTG	GCTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TGGCTGATGT	GCTTCTNCTG	180
CTTGAACCAG	AAGAGCAATC	TGTACTGCCT	GAAGCCGACC	ATCTGCTCCG	ACCAGGACAA	240
CTACTGCGTG	ACTGTGTCTG	CTAGTGCCGG	CATTGGGAAT	CTCGTGACAT	TTGGNCACAG	300
CTGAGCAAGA	CCTGTTNCCC	GGNCTGCCCC	ATNCG			335

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 641178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTTCGGGGA	GCTCGGCCAG	GCTGCTGGTA	CCTGCGTCCG	CCCGGCGAGC	AGGACAGGCT	60
GCTTTGGTTT	GTGACCTNCA	GGCAGGACGG	CCATCCTCTC	CAGAATGAAG	ATCTTNTTGC	120
CAGTGCTNCT	NGCTGCCCTT	CTGGGTGTGG	AGCGAGCCAG	CTNGCTGATG	TGCTTCTTCT	180
GCTTGAACCA	GAAGAGCAAT	CTGTACTGTC	TGAAGCCGAC	CATTGCTNCT	GACCAGGNCA	240
ACTACTGTGT	GACTGTNTNT	T				261

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 642012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCCGACCA	TCTGCTCCGA	CCAGGACAAC	TACTGCGTGA	CTGTGTCTGC	TAGTGCCGGC	60
ATTGGGAATC	TCGTGACATT	TGGCCACAGC	CTGAGCAAGA	CCTGTTCCCC	GGCTTGCCCC	120
ATCCCAGAAG	GCGTCAATGT	TGGTGTGGCT	TCCATGGGNA	TCAGCTGCTG	CCAGAGCTTT	180
CTGTGCAATT	TCAGTGCGGC	CGATGGCGGG	CTGCGGGCAA	GCGTCACCCT	GCTGGGTGCC	240
GGGCTGCTGC	TGAGCTGCTG	CCGGCCCTGC	TGCGGTTTGG	CCCCTGA		287

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGTUT02

(B) CLONE: 690697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGANGGTGG	GGGACCCANG	GGTCCGGCCA	NGGGTCCGAG	NTTCGGCAAG	GTNCTGGTAN	60
CTGCGTNCGG	CCGGCGAGCA	GGACANGNTG	CTTTGGTTTG	TGACTNCAGG	NAGGACGGCC	120
ATNCTTNCAG	AATTAAGATC	TTNTTGCCAG	TGCTGNTGGC	TGCCCTTCTG	GGTGTNGAGC	180
GAGCCAGTNG	NTGATGTGNT	TNTTCTGCTT	GAACCAGAAG	AGCAATCTGT	ACTGCCTGAA	240
GCCGACCATG	TGGTTCGACC	AGGGCAACTA	NTGCGTGACT	GTGTCTGTAG	TGNC	294

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGNOT03

(B) CLONE: 728784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCCAGAGCGC	GCGAGGTTCG	GGGAGCTCGG	CCAGGCTGCT	GGTACCTGCG	TCCGCCCCGC	60
GGACAGGCTG	CTTTGGTTTG	TGACCTCCAG	GCAGGACGGC	CATCCTCTCC	AGAATGAAGA	120
TCTTCTTGCC	AGTGCTGCTG	GCTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TCGCTGATGT	180
GCTTCTCCTG	CTTGAACCAG	AAGAGCAATC	TGTACTGCCT	GAAGCCGACC	ATCTGCTCCG	240
ACCAGGACAA	CTACTGNGTG	ACTGTG				266

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: OVARNOT03

(B) CLONE: 797584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TNGGNCCNGG	TGNTGGTACC	GNGTCCGCCC	GGCGAGCAGA	CAGGCTGCTT	TGGTTTGTGA	60
CCTCCAGGNA	GGACGGCCAT	CCTCTCCAGA	ATGAAGATCT	TCTTGCCAGT	GCTGCTGGCT	120
GCCCTTCTGG	GTGTGGAGCG	AGCCANCTCG	CTGATGTGCT	TCTCCTGCTT	GAACCAGAAG	180



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AGCAATCTGT ACTGCCTGAA GCCGACCATC TGCTNCGACC AGGNCAACTA CTGCGTGACT 240  
GTGTCTGCTA GTGCCGGCAT TGGGAATCTC GTGACAATTG 280

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT04
- (B) CLONE: 831396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTTNGGGGA GCTCCGTCAG GCTNCTGGTA CCTGCGTCCG CCCGGCGAGC AGGACAGGNT 60  
GCTTTANTTT NTGACCTNCA GGCAGGACGG CCATNCTATN CAGAATGAAG ATCTTATTGC 120  
CANTGCTGNT GGNTGNCCTT NTGNGTGTNG AGCGAGCCAG NTCNATGATG TGNTTNTCCT 180  
GNTTGAACCA GAAGAGCAAT NTGTANTGCC TGAAGCCGAC CATNTGNTCC GACCAGGACA 240  
ANTANTGCGT GANTGTGTNT GCTAGTGCCG GCATT 275

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT05
- (B) CLONE: 897330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAACCAGAAG AGCAATNTGT ACTGCCTGAA GCCGACCATN TGCTNCGACC AGGACAACCTA 60  
CTGCGTGACT GTGTNTGCTA GTGCCGGCAT TGGGAATNTN GTGACATTTG GCCACAGCCT 120  
GAGCAAGACC TGTTCCCNCG NCTGCCCCAT CCCAGAAGGC GTCAATGTTG GTGTGGNTTC 180  
CATGGGCATC AGCTGCTGCC AGAGCTTTNT GTGCAATTTT AGTGCGGCCG ATGGNNGGCT 240  
GNGGGCAAGC GTCACCN TGN TGGGTGCCCG GNTGNTGNTG AGCCTGGTGN CGGCCCT 297

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 509840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Met Lys Ala Phe Leu Phe Ala Val Leu Ala Ala Val Leu Cys Val Glu
 1          5          10          15
Arg Ala His Thr Leu Ile Cys Phe Ser Cys Ser Asp Ala Ser Ser Asn
          20          25          30
Trp Ala Cys Leu Thr Pro Val Lys Cys Ala Glu Asn Glu His Cys
          35          40          45
Val Thr Thr Tyr Val Gly Val Gly Ile Gly Gly Lys Ser Gly Gln Ser
          50          55          60
Ile Ser Lys Gly Cys Ser Pro Val Cys Pro Ser Ala Gly Ile Asn Leu
          65          70          75          80
Gly Ile Ala Ala Ala Ser Val Tyr Cys Cys Asp Ser Phe Leu Cys Asn
          85          90          95
Ile Ser Gly Ser Ser Ser Val Lys Ala Ser Tyr Ala Val Leu Ala Leu
          100          105          110
Gly Ile Leu Val Ser Phe Val Tyr Val Leu Arg Ala Arg Glu
          115          120          125
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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: UTRSN0T01

(B) CLONE: 588615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
ATGGCAGGCT TGGCCCTGCA GCCAGGNACT GCCCTGCTGT GCTACTCCTG CAAAGCCCAG      60
GTGAGCAACG AGGACTGCCT GCAGGTGGAG AACTGCACCC AGCTGGGGGA GCAGTGCTGG      120
ACCGCGCGCA TNCGGCAGTT GGCCTNCTGA CCGTCATCAG CAAAGGCTGC AGCTTGAAC      180
GCGTGGATGA CTNACAGGAC TACTACGTGG GCAAGAAGAA CATCACGTGC TGTGACANCG      240
ACTTGTGCAA NGGCANCGGG GCCCATGCCC TGCAGNCGGC TNTCGC      286
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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: UTRSN0T01

(B) CLONE: 590328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AANAGGTTAT	TAGGNGGGAA	NGAGGACNAN	NANGTGTGN	GACANCGACT	TGTGCAACGG	60
CAGCGGGGNC	CATGCCCTGN	AGCCGGCTGC	CGGCATCCTT	GCGCTGNTNC	CTGCACTCGG	120
NCTGCTGCTC	TGGGGACCCG	GNCAGCTATA	GGCTCTGGGG	GGNCCCGATG	CAGCCACAN	180
TGGGTGTGGT	GGCCCAAGGC	TTGTGGCANT	NNTAANAGAN	CTGGGNCCAG	TGGGAGGCTT	240
NTCTNGSTAA	A					251

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT02
- (B) CLONE: 1312529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACCATGA	AGGCTGTGCT	GCTTGCCCTG	TTGATGGCAG	GCTTGCCCTT	GCAGCCAGGC	60
ACTGCCCTGC	TGTGCTACTC	CTGCAAAGCC	CAGGTGAGCA	ACGAGGACTG	CCTGCAGGTG	120
GAGAACTGCA	CCCAGCTGGG	GGAGCAGTGC	TGGACCGCGC	GCATCCGCGC	AGTTGGCCTC	180
CTGACCGTCA	TCAGCAAAGG	CTGCAGCTTG	AACTGCGTGG	ATGACTCACA	GGACTACTAC	240
GTGGGCAAGA	AGAACATCAC	GTGCTGTGAC	ACCGACTTGT	GCAAGCCA		288

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT02
- (B) CLONE: 1314679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGCTGTGAC	ACCGACTTGT	GCAACGCCAG	CGGGGCCCCAT	GCCCTGCAGC	CGGCTGCCGC	60
CATCCTTGCG	CTGCTCCCTG	CACTCGGCCT	GCTGCTCTGG	GGACCCGGCC	AGCTATAGGC	120
TCTGGGGGGC	CCCGCTGCAG	CCCACACTGG	GTGTGGTGCC	CCAGGCCTCT	GTGCCACTCC	180
TCACAGACCT	GGCCAGTGG	GAGCCTGTCC	TGGTTCCTGA	GGCACATCCT		230

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

PF-0066 US

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BLADTUT02

(B) CLONE: 1315052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACCATGAA	GGCTGTGCTG	CTTGCCCTGT	TGATGGCAGG	CTTGGCCCTG	CAGCCAGGCA	60
CTGCCCTGCT	GTGCTACTCC	TGCAAAGCCC	AGGTGAGCAA	CGAGGACTGC	CTGCAGGTGG	120
AGAACTGCAC	CCAGCTGGGG	GAGCAGTGCT	GGACCGCGCG	CATCCGCGCA	GTTGGCCTCC	180
TGACCGTCAT	CAACAAAAGG	CTGCAGCTTG	AACTGCGTGG	ATGACTCACA	GG	232

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BLADTUT02

(B) CLONE: 1317088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGGGGCCCCAT	GCCCTGCAGC	CGGCTGCCGC	CATCCTTGCG	CTGCTCCCTG	CACTCGGCCT	60
GCTGCTCTGG	GGACCCG					77